

Patent Claims

1. Method for the multidimensional analysis of a proteome in which the biological material with the proteome to be analyzed is solubilized and the proteins belonging to the proteome are separated, quantitatively determined and identified, characterized in that the proteins of the proteome are subjected to a number n of different separating processes for $n > 2$ under standardized conditions in such a way that each of the liquid fractions m_1 obtained in a separating step supplies m_2 liquid fractions in a subsequent separating step, wherein, after n separating steps, there are $m_1 * m_2 * \dots * m_n = M$ liquid fractions which are identified by τ different analysis processes qualitatively and/or quantitatively by identification processes, known per se, and determined quantitatively by quantification processes which are likewise known per se, so that after combining the analysis data an n -dimensional image of the proteome is obtained which is characterized by identifiers and quantifiers and by the position in the n -dimensional data space.

2. Method according to claim 1, characterized in that methods which separate according to the size of the protein and/or methods which separate according to the mass of the protein and/or methods which separate according to the charge of the protein and/or methods which separate according to the hydrophobicity of the protein and/or methods which separate according to the shape of the protein and/or methods which separate according to the affinity of the protein, with respect to specific ligands, also to antibodies are selected as separating methods.

3. Method according to claim 1, characterized in that methods for determining specific immunological characteristics and/or methods for determining specific catalytic activity and/or methods for determining chemical modification of the proteins of the proteome are used as identification methods.

4. Method according to claim 1, characterized in that methods for nonspecific determination of protein concentration with different sensitivities

5. Method according to claim 1, characterized in that the identification of individual proteins of the proteome is carried out directly by mass determination of the proteins.

7. Method according to claim 1, characterized in that after the separation step the fractions are assembled in a two-dimensional multiple vessel system, preferably in the manner of and with the layout of microtitration plates.

9. Method according to claim 1, characterized in that all identification and quantification steps are carried out in a defined grid, preferably in the $n \times 96$ grid, with adaptable liquid handling technique.

11. Method according to claim 1, characterized in that the first dimension for separation is high-resolution size exclusion, ion exchange or hydrophobicity chromatography, which are known per se, in that the second dimension is carried out by parallel separation and fractionation of the fractions of

12. Method according to claim 1, characterized in that the analysis data for the n-dimensional image of the protein are assembled in a database.

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